Metabolic-related virulence traits in Streptococcus pneumoniae do not seem to be related with genomic differences

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Abstract

The gram-positive bacterium Streptococcus pneumoniae thrives in almost any environment. Under certain conditions this pathogen can cause several infections such as meningitis, otitis media, endocarditis or pneumonia. The virulence of a strain can be classified into 3 different levels: invasive, colonization and neutral.

The goal of this work was to uncover an eventual metabolic basis for these different levels of virulence. For that purpose, we tested if there was a connection between the presence of specific metabolic genes and virulence. For this, a dataset of DNA microarray data showing gene presence and absence and containing 1074 probes was used to analyze the DNA of 72 streptococcus strains, with different levels of virulence. The software Merlin was used to identify the metabolic pathways for each gene from the microarray data. For manipulation and reorganization of the microarray data the software Mev was used.

A Mann-Whitney test followed by a frame shift analysis were performed to analyse significant differences for each gene in each group of strains. The results show that around 50 genes were statistically different (predominantly present in invasive strains) between strain types. From these, only 10 were metabolic genes, which included functions such as an argininosuccinate synthase, an amino acid ABC transporter and a metabolic transposase.

According to the literature, 3 specific metabolic pathways are connected to virulence: purine metabolism, peptidoglycan biosynthesis and D-glutamine and D-Glutamate metabolism. In general there was not a large deviation in any of the pathways according to the virulence of the strains, hinting that the presence or absence of these specific pathways in the genome might not have a direct connection to virulence. It is thus likely that metabolic differences associated with virulence are not associated with genomic differences but rather with difference patterns in gene expression.